

Figure 5: SDS-PAGE showing expression of HAL in *E. coli*.

Lanes:

1 2X 3Z 4 B A

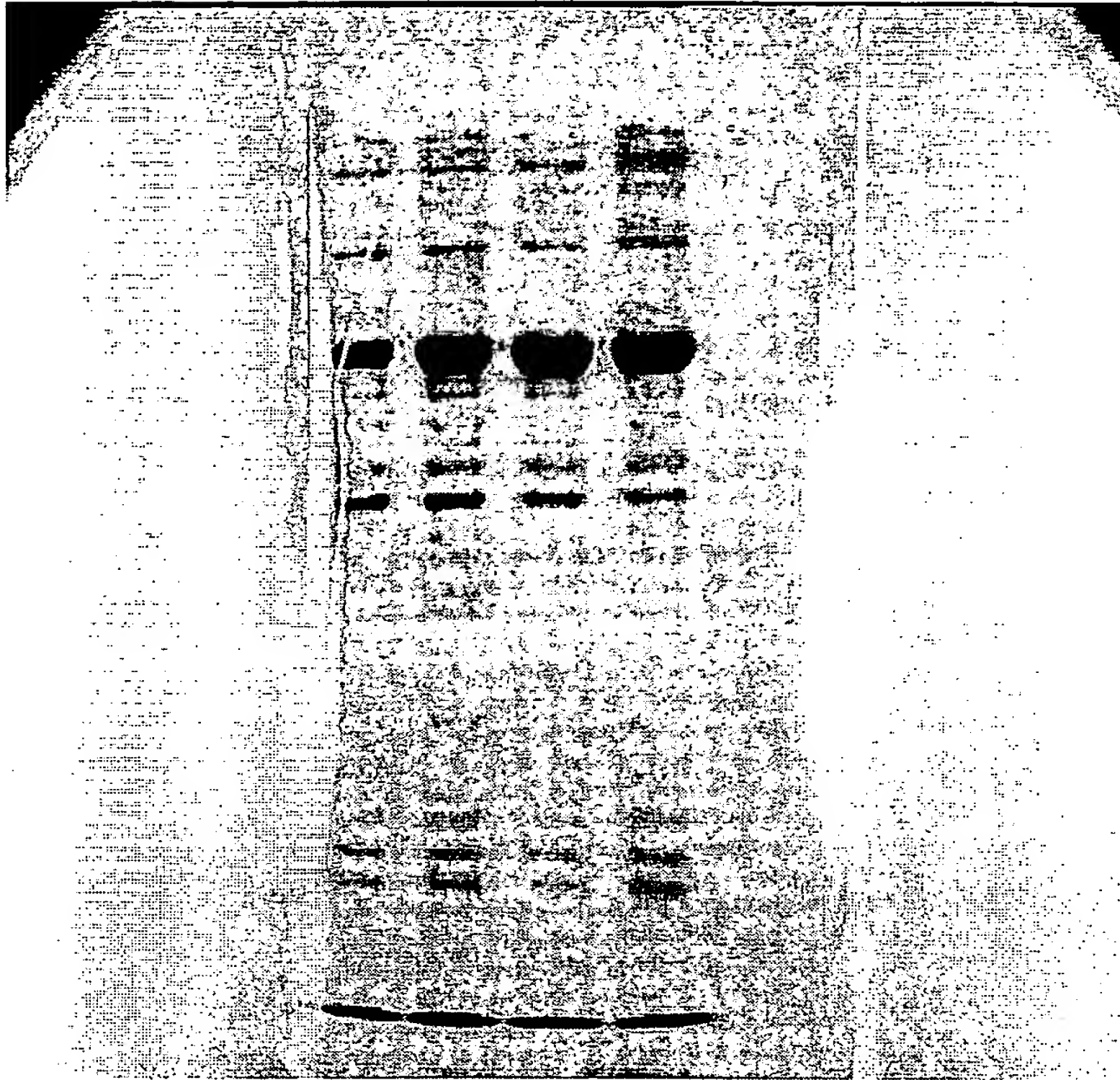
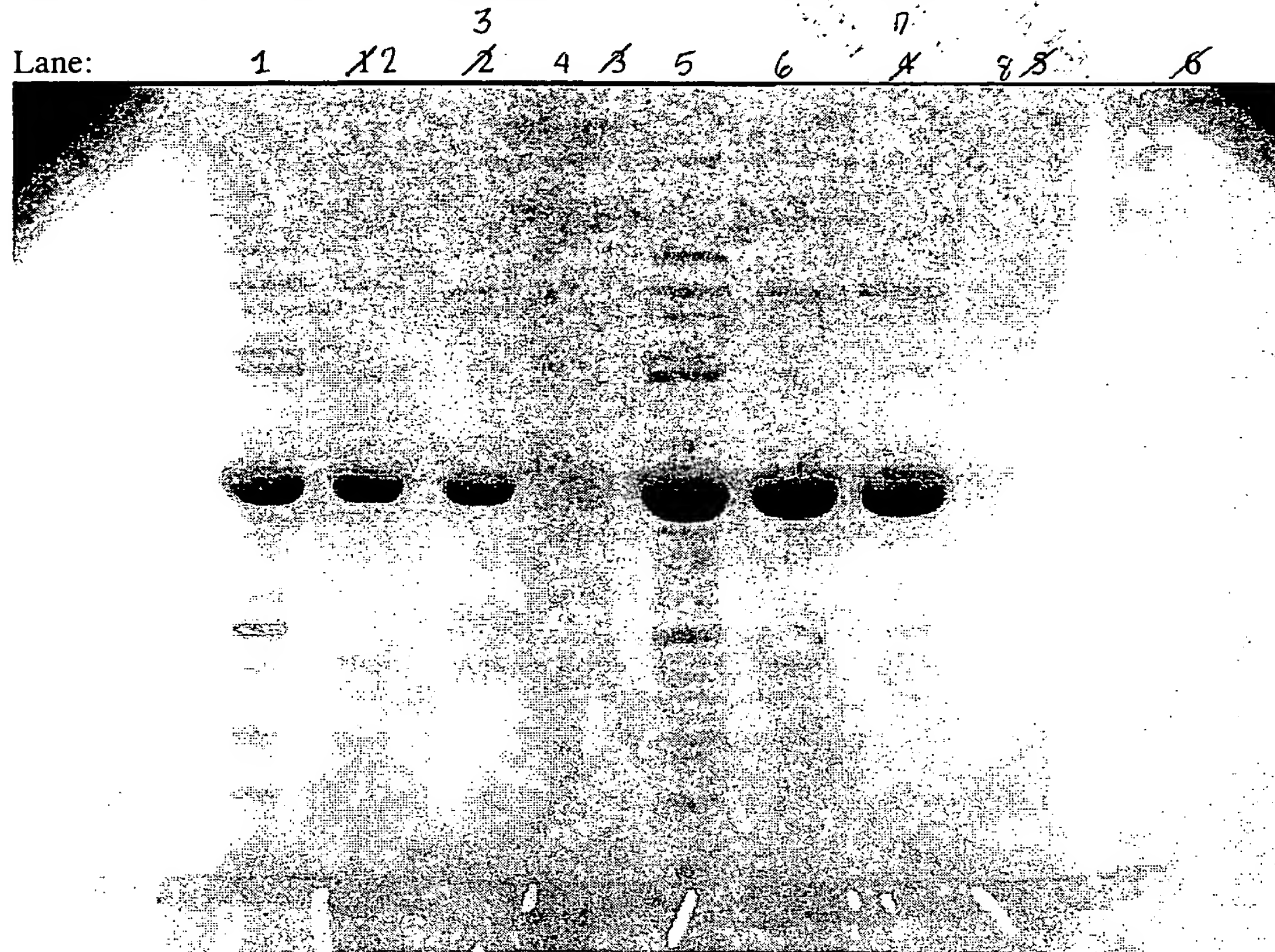




Figure 6: SDS-PAGE showing purification of HAL from *E. coli*



A
Figure 13: ~~Histidine ammonia lyase peptide sequence pileup~~

```
HUTH_PSEPU -----
-
HUTH_RHIME -----
-
HUTH_MOUSE
MPRYTVHVRGEWLAVPCQDGKLTVGWLGREAVRRYMKNKPDNGGFTSVDEVQFLVHRCKG
HUTH_RAT
MPRYTVHVRGEWLAVPCQDGKLSVGWLGREAVRRYMKNKPDNGGFTSVDEVRFVLRCKG
HUTH_HUMAN
MPRYTVHVRGEWLAVPCQDAQLTVGWLGREAVRRYIKNKPDNGGFTSVDDAHFLVRRCKG
HUTH_CAEEL      -MRLQVQIGTECVVVPCKP-DDTIHAVAKKSVEKLRRRLRPK----
LPLADDYFEVRRTVG
HUTH_BACS -----
-
HUTH_STRGR -----
-
HUTH_CORY -----
-

HUTH_PSEPU -----
-
HUTH_RHIME -----
-
HUTH_MOUSE      LGLLDNEDELEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_RAT        LGLLDNEDLLEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_HUMAN      LGLLDNEDRLEVALENNEFVEVVIEGDAMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_CAEEL
NSLLDPEDLVSDVLKDSDFIIVAASVEETEDAKEAKKQEEIDNARAEIEKIDNRRRKVSF
HUTH_BACS -----
-
HUTH_STRGR -----
-
HUTH_CORY -----
-

HUTH_PSEPU -----
TELTLKPGTTLTLAQLRAIHAAPVRLQLDASAAPAIIDASVACVEQIIA
HUTH_RHIME -----
MTVILRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVA
HUTH_MOUSE -----
EPEKYIALDGDSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIIK
HUTH_RAT -----
EPEKYIALDGDSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIIK
HUTH_HUMAN -----
EPEKYIELDGDRLTTEDLVNLGKGGRYKIKLTPTAEKRVQKSREVIDSIIK
HUTH_CAEEL
ADSLAPMVLAPPTKLLILDGNSLLPEDLVRCEKGECAIQLSMESEDRIKARTFLEKIAS
HUTH_BACS -----
MVTLDGSSLTTADVARVLFDFEEAAASEESMERVKKSRAAVERIVR
HUTH_STRGR -----
MDMHTVVVGTSGTAEDEVVAVARHGARVELSAAAVEALAAARLIVDALAA
HUTH_CORY -----
MASAPQITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALAS
```



^B
Figure 13 cont'd.

HUTH_PSEPU
EDRTAYGINTGFGLLASTRIASHDLENLQ RSLVLSHAAGIGAPLDDDLVRLIMVLKINSL
HUTH_RHIME
GNAPVYGINTGFGKLASIKIDSSDVATLQ RNLILSHCCGVGQPLTEDIVRLIMALKLISL
HUTH_MOUSE
ERTVVYGITTGFGKFARTVIPANKLQELQ VNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_RAT
ERTVVYGITTGFGKFARTVIPANKLQELQ VNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_HUMAN
EKTVVYGITTGFGKFARTVIPANKLQELQ VNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_CAEEL
EHRAVYGVTTGFGTFSNVTIPPEKLKKLQ LNLIRSHATGYGEPLAPNRARMLLALRINIL
HUTH_BACS
DEKTIYGINTGFGKFSDVLIQKEDSAALQ LNLILSHACGVGDPFPECVSRAMLLLRANAL
HUTH_STRGR
KPEPVYGVSTGFGALASRHIGTELRAQLQ RNIVRSHAAGMGRVEREVVRALMFLRLKTV
HUTH_CORY
ADTPVYGISTGFGALATRHIAPEDRAKLQ RSLIRSHAAGMGEPVEREVVRALMFLRAKTL

HUTH_PSEPU
SRGFSGIRRKVIDALIALVNAEVYPHIPL KGSVGASGDLAPLATMSLVLLGEGKARYKGQ
HUTH_RHIME
GRGASGVRLELVRLIEAMLDKGVIPLIPE KGSVGASGDLAPLAHMAAVMMGHGEAFFAGE
HUTH_MOUSE
AKGYSGISLETLKQVIEAFNASCLSYVPE KGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_RAT
AKGYSGISLETLKQVIEVFNASCLSYVPE KGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_HUMAN
AKGYSGISLETLKQVIEMFNASCLPYVPE KGTVGASGDLAPLSHLALGLVGEKGMWSPKS
HUTH_CAEEL
AKGHSGISVENIKKMIAAFNAFCVSYVPQ QGTVGCSGDLCPAHLALGLLGEGKMWSPTT
HUTH_BACS
LKGFSGVRAELIEQLLAFLNKRVPVIPPQ QSLGASGDLAPLSHLALALIGQGEVFFEGE
HUTH_STRGR
ASGHTGVRPEVAQTMADVNLNAGITPVVH EYGS LGCSGDLAPLSHCALTMGEGEAEGPDG
HUTH_CORY ASGRS-
VRPVVLETMVGMLNAGITPVVREYGS LGCSGDLAPLSHCALVLMGEGEATDAHG

HUTH_PSEPU -
WLSATEALAVAGLEPLTLAAKEGLALLNG TQASTAYALRGLFYAEDLYAAAIACGGLSV
HUTH_RHIME -
RMKGDAALKAAGLSPVTLAAKEGLALINGT QVSTALALAGLFRAHRAGQAALITGALST
HUTH_MOUSE
GWADAKYVLEAHGLKPIVLKPKEGLALINGT QMITS LGCEALERASAIARQADIVAALT
HUTH_RAT
GWADAKYVLEAHGLKPIVLKPKEGLALINGT QMITS LGCEAVERASAIARQADIVAALT
HUTH_HUMAN
GWADAKYVLEAHGLKPVILKPKEGLALINGT QMITS LGCEAVERASAIARQADIVAALT
HUTH_CAEEL
GWQPADVVLKKNLEPLELGPKEGLALINGT QMTALGAYTLERAHNIARQADVIAALS
HUTH_BACS -
RMPAMTGLKKAGIQPVTLT SKEGLALINGT QAMTAMGVVAYIEAEKLAYQTERIASLTI
HUTH_STRGR
TVRPAGELLA AHGIAPVELREKEGLALLNGT DGMLGMLVMALADLRNLYTSADITAALS
HUTH_CORY
DIRPVPELFAEAGLTPVELAEKEGLALVNGT DGMLGQLIMALADLDELDDIADATAAMSV



Figure 13 cont'd.

HUTH_PSEPU EAVLGSRSPFDARIHE-ARGQRGQIDTAACFRDLLGDSSEVSLSHKNCD----
KVQDPYS
HUTH_RHIME DAAMGSSAPFHPDIQH-CAAIRARSTRAAALRQLLTG-SPIRQSHIEGDE---
RVQDPYC
HUTH_MOUSE EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_RAT EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_HUMAN EVLKGTTKAFDTDIHA-LRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_CAEEL DVLKGTTRAYDPDIHR-IRPHRGQNL SALRLRALLHS-
EANPSQIAESHRNCTKVQDAYT
HUTH_BACS EGLQGIIDAFDEDIHL-ARGYQEQIDVAERIRFYLS-GLTTSQGE-----
LRVQDAYS
HUTH_STRGR EALLGTDKVLAPELHA-IRPHPGQGV SADNMSRVLAG-SGLTGHHQDDAP---
RVQDAYS
HUTH_CORY EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMFAFLAD-SPIVASHREGDG---
RVQDAYS

HUTH_PSEPU
LRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPVAMAADNL
HUTH_RHIME IRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLVLSDN-
SVVSGGNFHAEPVAFADQI
HUTH_MOUSE
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_RAT
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_HUMAN
LRCCPQVHGVVNDTIAFVKNIITTELNSATDNPMVFANRGETVSGGNFHGEYPAKALDYL
HUTH_CAEEL
LRCVPQVHGVVHDTIEFVREIITTEMNSATDNPLVFADREEIISGGNFHGEYPAKALDFL
HUTH_BACS
LRCIPQVHGATWQTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGQPIAFAMDFL
HUTH_STRGR VRCAPQVNGAGRDTLDHAALVAGRELASSVDNPVVLPGD-
RVESNGNFHGAPVAYVLDFL
HUTH_CORY LRCSPQVTGAARDTIAHARLVATRELAAAIDNPVVLPSG-
EVTSNGNFHGAPVAYVLDFL

HUTH_PSEPU ALAIAEIGSLSERRISLMDKHMS-
QLPPFLVNGGVNSGFMIAQVTAAALASENKALSH
HUTH_RHIME
ALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLSGLMIAEVTSAALMSENKQLSH
HUTH_MOUSE AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_RAT AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_HUMAN AIGIHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSENKALCH
HUTH_CAEEL AIAVAELAQMSERRRLRLVNKELS-
GLPTFLTPDGGLNSGFMIVQLCAASLVSENKVLCH
HUTH_BACS KIAISELANIAERRIERLVNPQLN-
DLPPFLSPHPGLQSGAMIMQYAAASLVSENKTLAH
HUTH_STRGR
AIVAADLGSICERRTRDLLDKNRSHGLPPFLADDAGVD SGLMIAQYTQAALVSEMKRLAV
HUTH_CORY
AIAVADLGSIAERRTRDMLDPAARSRLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV



D
Figure 13 cont'd.

HUTH_PSEPU PHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG-LKTS
HUTH_RHIME PASVDSTPTSANQEDHVSMACHGARLLQMTENLFSIIGIEALAAVQGIEFRAP-LTTS
HUTH_MOUSE PSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_RAT PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_HUMAN PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_CAEEL PSSVDSIPTSCNQEDHVSMGGFAARKALTVVEHVEAVLAMELLAACQGIEFLKP-LIST
HUTH_BACS PASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGI-EHAA
HUTH_STRGR
PASADSI PSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGGLTPA
HUTH_CORY PA-VDSIPSSAMQEDHVSLGWAARKLPTSVANLRRILAVEMLIAGRALDLRAP-LKPG

HUTH_PSEPU AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAKG---S-LTGLLPAGVLPSTL---

HUTH_RHIME PELQKAAAVRGVSS-SIEEDRYMADDLKAAGDLVASG---R-LAAAVSAGILPKLEN-

HUTH_MOUSE TPLEKVYDLVRSVVR-

PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR

HUTH_RAT TPLEKVYDLVRSVVR-

PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR

HUTH_HUMAN TPLEKVYDLVRSVVR-

PWIKDRFMAPDIEAAHRLLEQKVWEVAAPYIEKYRMEHIPESR

HUTH_CAEEL APLHKIYQLVRSVAP-

PLNEDRYMKPEIDAVLEMIRENRIWEAVLPHLETLEAMEELDPD

HUTH_BACS SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKK----ESLIPDHQNKELRGMNI-

HUTH_STRGR PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREG---R-LVAAVEPVTGPLA---

HUTH_CORY PATGAVLEVLRSKVA-GPGQDRFLSAELEAAYDLLANG---S-VHKALEAHLPE-----

HUTH_PSEPU -----

HUTH_RHIME -----

HUTH_MOUSE PLSPTAFSLES LRKNSATIPESDDL----

HUTH_RAT PLSPTAFSLES LRKNSATIPESDDL----

HUTH_HUMAN PLSPTAFSLQFLHKKSTKIPESDL----

HUTH_CAEEL ALRQFTKTPTGIVQDRSMIPISDDEESIE

HUTH_BACS -----

HUTH_STRGR -----

HUTH_CORY -----

Figure 14 A

983831	100.0%	1	
1 SWALL: CAC21618	66.1%		
2 SWALL: HUTH_STRGR	65.4%		
3 SWALL: HUTH_DEIRA	46.8%		
4 SWALL: BAB16159	42.0%		
5 SWALL: Q9KWE4	42.0%		
6 SWALL: HUTH_BACSU	40.4%		
7 SWALL: Q9KSQ4	42.2%		
8 SWALL: Q9HU85	41.7%		
9 SWALL: Q9KBE6	39.3%		
10 SWALL: HUTH_PSEPU	41.7%		
11 SWALL: HUTH_RHIME	40.6%		
12 SWALL: Q9HU90	40.7%		
13 SWALL: HUTH_HUMAN	39.2%		
14 SWALL: HUTH_CAEEL	38.8%		
15 SWALL: Q9HLI6	41.0%		
16 SWALL: HUTH_MOUSE	38.6%		
17 SWALL: BAB29407	38.6%		
18 SWALL: HUTH_RAT	38.2%		
19 SWALL: AAG53586	39.8%		
20 SWALL: Q9KKE0	38.9%		
21 SWALL: Q9HQD5	42.2%		

[

MASAPQITLGLSGATADDVIAVARHEARISISPVLEELASVRAHIDALASADTPVYGISTGFGALATRHIAPEDRAKLQ
---MHTVVVGTSVGTASDVLAVARAGARIELSEEAVALAAARSVVDALAAKPDVYGVSTGFGALATRHISPELRGRLO
-MDMHTVVVGTSVGTAEDEVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGALASRHIGTELRAQLO
-----MILDRDLNLEQFISVVRHGEQVELSAAARERARARTVIEQIVEGDTPIYGVNTGFGKFENVQIDRSQLAQLO
-----VPLHHLADIYWNNGSAKLDPSFDDAVALKGAARIAEIAAGNAPVYGINTEGFKLASIKIDAADLALTLQ
-----VPLHHLADIYWNNGSAKLDPSFDDAVALKGAARIAEIAAGNAPVYGINTEGFKLASIKIDAADLALTLQ
-----MVTLDGSSLTTADVARVLFDFEEAAASESMERVKKRAAVERIVRDEKTIYGINTEGFKFSDVLIQKEDSAAALQ
---MLHLMIKPGQLSLKQLRQVSRSPVLSLDPEAIPAIAESAQVVEQVISEGRTVYGINTEGFKLLANTKIAPODLETLQ
---MSHLKPGQLTLADLRQAYLAPVRLSLDPSADAPIAASVACVENIIAEGRTAYGINTEGFKLLASTRISPADLEKLO
---MTNLKLLDGRSLSLHDLHRIIYEGETVGASDESMKVKQSRKAVEQIVADEKIIYGITTEGFKFSDIFIDPDDVENLO
---TELTLKPGTLTLAQLRAIHAAPVRLQDASAPADAIDASVACVEQIIAEDRTAYGINTEGFKLLASTRIASHDLENLO
-----LRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVAGNAPVYGINTEGFKLASIKIDSSDVATLO
MSDLPVSVFGDPLRWQELVAVARHGARLELSAAAWARIDNARAIVCRIVANGERAYGISTGLGALCDVLLLEGEQLAELS
KYREPEKYIELDGLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIKEKTVVYGITTEGFKFA-RTVPIPNKLQLO
VLAPTKLLILDGNSPEDLVRCCKECAIQLSMESEDRIRKARTFLEKIASEHRAVYGVTTGFTFSNVTIPEKLLKLO
-----MIEIDGRSLRVEDVYAVAVEYDRVSISSDRTLKAVEEKHEAFLKINSKTVYGVNTGFGSLLNVHIERDQEILO
KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSAIEKKVQKSREVIDSIIKERTVVYGITTEGFKFA-RTVPIPNKLQLO
KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSAIEKKVQKSREVIDSIIKERTVVYGITTEGFKFA-RTVPIPNKLQLO
KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSAIEKKVQKSREVIDSIIKERTVVYGITTEGFKFA-RTVPIPNKLQLO
---MNALTLTPGTLTLAQLRQVWQQLTLDESHEAINDSVACVEAIVAEGRAYGINTEGFKLLAQTRIAHDLENLO
---MGEMISLDGPLTWREIASIAEGASLDLSPARLRIAQAARRIVDALVERGIRGYGINTEGFKALCDVIIISRENQQALS
-----MSDTRIDAADREALQ

80

Figure 14³ cont'd.

	81		160
983831	100.0%		[
1 SWALL:CAC21618	66.1%		RSLIRSHAAGMGEVEREVVRALMFLRAKTLASGRTGVRPVVLETMVGMNLNAGITPVVREYGSGLGSCGDLAPLSHCALVL
2 SWALL:HUTH_STRGR	65.4%		RNIVRSHAAGMGEPRVEREVVRALMFLRLKTVCSGRTGVRPEVAQTMADVNLNAGITPVVHEYGSGLGSCGDLAPLSHCALT
3 SWALL:HUTH_DEIRA	46.8%		RNIVRSHAAGMGEPRVEREVVRALMFLRLKTVASGHTGVRPEVAQTMADVNLNAGITPVVHEYGSGLGSCGDLAPLSHCALT
4 SWALL:BAB16159	42.0%		HNLIIVSHAIGMGEPLPAEVVRGMLLRAQSLSLCHSGVRVEVELLALLNADALPVVPQSGSVGASGDLAPLAHLALGL
5 SWALL:Q9KWE4	42.0%		RNLIILSHCCGVGAPLPENVRRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVPEKGSVGSAGDLAPLAHMSATM
6 SWALL:HUTH_BACSU	40.4%		RNLIILSHCCGVGAPLPENVRRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVPEKGSVGSAGDLAPLAHMSATM
7 SWALL:Q9KSQ4	42.2%		LNLIILSHACGVDPFPECVSRAMLLLRANALLKGFSGVRAELIEQLLAFNKRHPVIPPQQGSLGASGDLAPLSHLALAL
8 SWALL:Q9HU85	41.7%		KSIVLSHAAGIGELMSDETURLMMLLKINSLARGYSGIRLEVIQALIELVNNQIYPCVPKKGSGVGSAGDLAPLAHMSATM
9 SWALL:Q9KBE6	39.3%		RSIVLSHAAGVGEALDDAMVRLVMLLKVNLSLARGFSGIRRKVIDALIALINAEVYPHIPKKGSGVGSAGDLAPLAHMSATM
10 SWALL:HUTH_PSEPU	41.7%		HNLIYSHACGVSPFETVSRMTMLVRANALLKGFSGVRPLVIERLLALVNANIHPVIPPQQGSLGASGDLAPLSHLALVL
11 SWALL:HUTH_RHIME	40.6%		RSLVLSHAAGIGAPLDDDLVRLIMVLLKINSLSRGSGIRRKVIDALIALVNAEVYPHIPKKGSGVGSAGDLAPLAHMSATM
12 SWALL:Q9HU90	40.7%		RNLIILSHCCGVGQPLTEDIVRLIMALKLISLGRGASGVRLIEAMLDKGVIPVPEKGSVGSAGDLAPLAHMAAVM
13 SWALL:HUTH_HUMAN	39.2%		RNTLLSHACGVGEPLRDEQTRAIICAAVANYSQKSGLDRLSVEGLLALLNHGITPQVPAQGSVGY---LTHMAHVGI
14 SWALL:HUTH_CAEEL	38.8%		VNLVRSHSSGVGKPLSPERCRLMALLRINVLAKGYSGISLETQKQVIEFMFNASCLPYVPEKGTGASGDLAPLSHLALGL
15 SWALL:Q9HLI6	41.0%		LNLIIRSHATGYGEPLAPNRARMMLLALRINILAKGHSGISVENIKKMIAFNFCVSVYPQQTGTVGSCGDLAPLAHLALGL
16 SWALL:HUTH_MOUSE	38.6%		KNLIIRSHSSGVGDYLENRYVRAIMAVRLNSLAAGYSVAVSADLLNMVEMLNRDVIPAIPKYGSVGSAGDLAPLAHIGLAM
17 SWALL:BAB29407	38.6%		VNLVRSHSSGVGKPLSPERCRLMALLRINVLAKGYSGISLETQKQVIEAFNASCLSYVPEKGTGASGDLAPLSHLALGL
18 SWALL:HUTH_RAT	38.2%		VNLVRSHSSGVGKPLSPERCRLMALLRINVLAKGYSGISLETQKQVIEAFNASCLSYVPEKGTGASGDLAPLSHLALGL
19 SWALL:AAG53586	39.8%		RSLVLSHAAGVGEPLDDDIVRLMMVLKINSLARGFSGIRLSVIOALIALVNAGVSVDPKAGSVGSAGDLAPLAHMSATM
20 SWALL:Q9KKE0	38.9%		RNLIILSHACGVGDPLGRVEARAVMAAQIANLTHGYSGVVRVETAEMLLALLNADIIPVPSRGSVGY-----LTHAALVL
21 SWALL:Q9HQD5	42.2%		ANLVRSHAAGAGSELDTAAVRALLVTRNLALAKGYSGIRERVLVDVLVGLLNEGVPVPSRGSVGSAGDLAPLAHMSATM

Figure 14, cont'd.

	161	2	240
983831	100.0%		MGEGEATDAHGDIRVPPELFAEAGLTPVELAEKEGLALVNGTDGMLGQIMALADLDELDDIADATAAMSVEAQLGTDQV
1 SWALL:CAC21618	66.1%		MGEEDAEGPDGTVRPAGELLAHAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLDTLYKSADITAAALTMEALLGTDV
2 SWALL:HUTH_STRGR	65.4%		MGEGEAEGPDGTVRPAGELLAHAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLNRNLYTSADITAAALSLEALLGTDKV
3 SWALL:HUTH_DEIRA	46.8%		IGLGD I-EYQGVQVRPAADVLAELGLSPVQLQAKEGLALINGTQLMGSLALALHDAQVLLGTANLAAAMTVARYGSHRP
4 SWALL:BAB16159	42.0%		MGEGEAF-YQGVQMPKDALAKAGLSPVLAKEGLALINGTQSTALALAGLFRHRAAQSAQSVLVTGALSTDAAMGSSAP
5 SWALL:Q9KWE4	42.0%		MGEGEAF-YQGVQMPKDALAKAGLSPVLAKEGLALINGTQSTALALAGLFRHRAAQSAQSVLVTGALSTDAAMGSSAP
6 SWALL:HUTH_BACSU	40.4%		IGQGEVF-FEGERPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEKLAQYQTERIASLTIEGLQGIIDA
7 SWALL:Q9KSQ4	42.2%		LGEQAR-YNGKIIISGLEAMKIAGLEPITLAPKEGLALLNGTQASTAFALGLEGLFVAEDLFASATVCGAMSVEAALGSRRP
8 SWALL:Q9HU85	41.7%		IGESRARH-RGEWLPAAEALAVAGLEPLTLAAKEGLALLNGTQVSTAYALRGLFEAEDLFAAATVCGGLSVEAMLGSRAP
9 SWALL:Q9KBE6	39.3%		LGEGEVF-YKGTKTAKASFALKEEIEPITLTAKEGLALINGTQAMTAMGVVAYIEAEKLAQYQSEIIASLTMEGLRGIIDA
10 SWALL:HUTH_PSEPU	41.7%		LGEQKAR-YKGQWLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFEAEDLFAAATVCGGLSVEAALGSRSP
11 SWALL:HUTH_RHIME	40.6%		MGHGEAFFAGERMKGDAALKA-AGLSPVTLAAKEGLALINGTQVSTALALAGLFRHRAQQAALITGALSTDAAMGSSAP
12 SWALL:Q9HU90	40.7%		LGIGEV S-YRGSVVPAAALAAEGLATVRLGAKDGLCLVNGTQPCMTGLACALDQORLAQWADVIGAMSFALRGQLAA
13 SWALL:HUTH_HUMAN	39.2%		VGEKMWSPKSGWADAKYVLEAHGLKPVILKPKKEGLALINGTQMTSLGCEAVERASAIARQADIVAAALTLEVLKGTTKA
14 SWALL:HUTH_CAEEL	38.8%		LGEKMWSPKSGWADAKYVLEAHGLKPVILKPKKEGLALINGTQMTSLGCEAVERASAIARQADIVAAALTLEVLKGTTKA
15 SWALL:Q9HLI6	41.0%		MGEKAF-FEGRMDSARALEKAGLKPYPQFKEKEGVALINGTQMTSLGCEAVERASAIARQADIVAAALTLEVLKGTTKA
16 SWALL:HUTH_MOUSE	38.6%		IGEGKMWSPKSGWADAKYVLEAHGLKPVILKPKKEGLALINGTQMTSLGCEAVERASAIARQADIVAAALTLEVLKGTTKA
17 SWALL:BAB29407	38.6%		IGEGKMWSPKSGWADAKYVLEAHGLKPVILKPKKEGLALINGTQMTSLGCEAVERASAIARQADIVAAALTLEVLKGTTKA
18 SWALL:HUTH_RAT	38.2%		IGEGKMWSPKSGWADAKYVLEAHGLKPVILKPKKEGLALINGTQMTSLGCEAVERASAIARQADIVAAALTLEVLKGTTKA
19 SWALL:AAG53586	39.8%		LGEQKAR-YRGEWLPAAALQKAGLAPVTLAAKEGLALLNGTQASTAFALRGLFEAEDLFASAVVCGALTTEAVLGSRRP
20 SWALL:Q9KKE0	38.9%		IGHGSAMQGTTERLSGADAL-ARLGLAPLRLEAKEGLSLVNGTQCATGLAALALARTERLFAWADAAAAMTYE-NLGSQAN
21 SWALL:Q9HQD5	42.2%		IGEGQA-DVAGERMPAAEALAAADLEPVTLOAKEGLALINGTQLTGTGVAALALVDAERVLSADTAGALTTEVTMSTTAS

Figure 14₂ cont'd.

	983831	241		3	320
1	SWALL: CAC21618	100.0%	[FRAELHEPLRPHPGQGRSAQNMFADSPIVASHREGDGRVQDAYSLRCSQVGTGAARDTIAHARLVATRELAAIDNP	
2	SWALL: HUTH_STRGR	66.1%		LAPELHA-IRPHPGQAASAAANMAAVLKSGSLTGHQDDAPRVQDAYSVRCAPQVAGAGRDTMAHAGLVAERELAAAVDNP	
3	SWALL: HUTH_DEIRA	65.4%		LAPELHA-IRPHPGQGVSAADNMSRVLAGSGLTGHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAALVAGRELASSVDNP	
4	SWALL: BAB16159	46.8%		FQPDV-VGLRPHPGALAVAAELREFLAGSEIAPSHLTGDKGVQDAYSLRAVPQVHGATWDALAQAEVLAVEFASVTDNP	
5	SWALL: Q9KWE4	42.0%		FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCQPVQVAGACLDLLASVARTLEIEANAVTDNP	
6	SWALL: HUTH_BACSU	42.0%		FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCQPVQVAGACLDLLASVARTLEIEANAVTDNP	
7	SWALL: Q9KQSQ4	40.4%		FDEDIHLA-RGYQEIQIDVAERIRFYLSDSLTT--QGELRVQDAYSLRCPQVQVAGACLDLLASVARTLEIEANAVTDNP	
8	SWALL: Q9KHU85	42.2%		FDPRIHR-VRGHRTOMDAATAYRHLLVSSSEIGQSHNCE-KVQDPYSLRCPQVQVAGACLDLLASVARTLEIEANAVTDNP	
9	SWALL: Q9KBE6	41.7%		FDARIHAA-RGQRGQIDVAAAYRDLLASSEVARSHKCD-KVQDPYSLRCPQVQVAGACLDLLASVARTLEIEANAVTDNP	
10	SWALL: HUTH_PSEPU	39.3%		FDEQIHFA-RGYVEQVDVARRMESYLQDSQTT--RQELRVQDAYSLRCPQVQVAGACLDLLASVARTLEIEANAVTDNP	
11	SWALL: HUTH_RHIME	41.7%		FDARIHEA-RGQRGQIDTAACFRDLLGDSSEVSSHKNCD-KVQDPYSLRCPQVQVAGACLDLLASVARTLEIEANAVTDNP	
12	SWALL: Q9HU90	40.6%		FHPDIQHCAAIRARSTRAAA-LRQLLTGSPIRQSHIEGDERVQDPYCIRCQPVQVAGACLDLLASVARTLEIEANAVTDNP	
13	SWALL: HUTH_HUMAN	40.7%		FDAEI-VALKPHPGMQRVAANLRALLAGSQVLENAR--GIRTQDALSIRSIPQIHGACRDLAHARQIET-ELNSATDNP	
14	SWALL: HUTH_CAEEL	39.2%		FDTDIHA-LRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGAVVNDTIAFVKDIIITTELNSATDNP	
15	SWALL: Q9HLI6	38.8%		YDPDIHR-IRPHRGQNLALRLRALLNPSQIAESHRNCT-KVQDAYTLRCPQVQVAGACLDLLASVARTLEIEANAVTDNP	
16	SWALL: HUTH_MOUSE	41.0%		FTPWILGA-RPHLGQVAIGNRFREYLTGSDIV--KRADSVKVQDAYTLRCPQVYGSVADVIDYVENVLSVEINSATDNP	
17	SWALL: BAB29407	38.6%		FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGAVVNDTIAFVKDIIITTELNSATDNP	
18	SWALL: HUTH_RAT	38.6%		FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGAVVNDTIAFVKDIIITTELNSATDNP	
19	SWALL: AAG53586	38.2%		FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGAVVNDTIAFVKDIIITTELNSATDNP	
20	SWALL: Q9KKE0	39.8%		FDARIHE-VRGQRGQIDAAALFRHVLTDTSAIAASHHNCNCD-KVQDPYSLRCPQVQVAGACLDLLASVARTLEIEANAVTDNP	
21	SWALL: Q9HQD5	38.9%		AFAPLALRQSPGLSAGGELRDWLADSPMLAG--TAGTRTQDPLSLRAVPQVHGAAARDAFGQVAEIVDRELASVTDNP	
		42.2%		CAPAIHE-VRPHDGGQAVSARHIRNLTAGSEVLDHHRDCD-RVQDAYSLRCPQVHGAVRDALDHLRAAVATELNSATDNP	

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Figure 14, cont'd.

983831	321	100.0%	VVLPSGEVTSNGNFHGA	400
1 SWALL: CAC21618	100.0%	66.1%	VVLPGRVEVTSNGNFHGA	
2 SWALL: HUTH_STRGR	65.4%	46.8%	LIFPTGEVSVSGNFHGA	
3 SWALL: HUTH_DEIRA	46.8%	42.0%	LVLSDNSVSVSGNFHGA	
4 SWALL: BAB16159	42.0%	42.0%	LVLSDNSVSVSGNFHGA	
5 SWALL: Q9KWE4	42.0%	40.4%	LIFNDGDVSVSGNFHGA	
6 SWALL: HUTH_BACSU	40.4%	42.2%	LVFADGDIISGDNFHA	
7 SWALL: Q9KSQ4	42.2%	41.7%	LVFAAGDVSVSGNFHA	
8 SWALL: Q9HU85	41.7%	39.3%	LIFDNGQVSVSGNFHGA	
9 SWALL: Q9KBE6	39.3%	41.7%	LVFAAGDVSVSGNFHA	
10 SWALL: HUTH_PSEPU	41.7%	40.6%	LVLSDNSVSVSGNFHA	
11 SWALL: HUTH_RHIME	40.6%	40.7%	LLLGTPVSVQANPHGE	
12 SWALL: Q9HU90	40.7%	39.2%	MVFANGETVSVSGNFH	
13 SWALL: HUTH_HUMAN	39.2%	38.8%	LVFADREIISGDNFHA	
14 SWALL: HUTH_CAEEL	38.8%	41.0%	L-FNGEEVSVSGNFHG	
15 SWALL: Q9HLI6	41.0%	38.6%	MVFASGETISGDNFHA	
16 SWALL: HUTH_MOUSE	38.6%	38.6%	MVFASGETISGDNFHA	
17 SWALL: BAB29407	38.6%	38.2%	MVFASGETISGDNFHA	
18 SWALL: HUTH_RAT	38.2%	39.8%	LVFAANEMVFRGNFHA	
19 SWALL: AAG53586	39.8%	38.9%	AVAGSPEVHSQAHVGA	
20 SWALL: Q9KKE0	38.9%	42.2%	LVFPGTGVSVSGNFHG	
21 SWALL: Q9HQD5	42.2%			

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Figure 14, cont'd.

	983831	401	480
1	SWALL: CAC21618	100.0%	NKRLAVPASVDSIPSSAMQEDHVS LGWHAARKLRTSVANLRRILAVEMLIAGRALDLRAPLKP GPATGAVLEVLR SKVAG
2	SWALL: HUTH_STRGR	66.1%	LKRLAVPASADSIPSSAMQEDHVS MGWSAARKLRTAVDNLARVIAVELYAAATRAIQ LREGLT PAPASQAVVEAVRAAVEG
3	SWALL: HUTH_DEIRA	65.4%	MKRLAVPASADSIPSSAMQEDHVS MGWSAARKLRTAVDNLARIVAVELYAAATRAIELRAALT PAPASEAVVAALRAAGAG
4	SWALL: BAB16159	46.8%	NKVL SHPASVDSIPT SANQEDHVS MGHAARQLRQIVANQTVLSIELLCAQQGLDFQQ-LRAGRGVQAAEYVRTFVPT
5	SWALL: Q9KWE4	42.0%	NKQMSHPASVDSIPT SANQEDHVS MACHGARRLLAMTDNLF GILGIEALAAVQGVELRGPLKTSPELEKAAAVLRSAPV
6	SWALL: HUTH_BACSU	42.0%	NKQMSHPASVDSIPT SANQEDHVS MACHGARRLLAMTDNLF GILGIEALAAVQGVELRGPLKTSPELEKAAAVLRSAPV
7	SWALL: Q9KSQ4	40.4%	NKTLAHPASVDSIPT SANQEDHVS MGTHAARHAYQVIANTRRVIAIEAICALQAVEYRGIEHAASYTKQLFQEMRKVVPS
8	SWALL: Q9HU85	42.2%	NKTLAHPASVDSIPT SANQEDHVS MATFAARRLRDMGENTRGILAVEYLAAQQGLDFRAPLKSSPRIEEARQILREKVPF
9	SWALL: Q9KBE6	41.7%	NKALAHPASVDSIPT SANQEDHVS MAPNAGKRLWAMAENVRGILAVEWLGACQGLDFREGKSSPKLEQARRLLRDKVPY
10	SWALL: HUTH_PSEPU	39.3%	NKTLAHPASVDSIPT SANQEDHVS MGTHGSRHAYQIIQNVRNVLAIEILICAMQAVDIRGREKMASFTKKILEKGREHVPY
11	SWALL: HUTH_RHIME	41.7%	NKALSHPHSVDSIPT SANQEDHVS MAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLRKGLKTSAKLEKARQALRSEVAH
12	SWALL: Q9HU90	40.6%	NKQLSHPASVDSIPT SANQEDHVS MACHGARRLLQMTENLFSIIGIEALAAVQGVIEFRAPLTTSP ELQKAAAARGVSSS
13	SWALL: HUTH_HUMAN	40.7%	NRQLAQPAVVDNFVTSALQEDHLSLGTSAALKLGRALENLRRILAEIYLLAAQAFELAPQRFQGTAAAGILRERVPA
14	SWALL: HUTH_CAEEL	39.2%	NKALCHPSSVDSIPT SANQEDHVS MGWGAARKALRVIEHVEQVLAIELLAACQGI EFLRPLKTTT PLEKVYDLVRSVVRP
15	SWALL: Q9HLI6	38.8%	NKVLCHPSSVDSIPT SANQEDHVS MGWGAARKALRVIEHVEQVLAIELLAACQGI EFLRPLKTTT PLEKHIIYQLVRS-VAP
16	SWALL: HUTH_MOUSE	41.0%	NKVLAYPSSADTIPT SANQEDHVS MGATGSLKLEIIDNVRYIIAIEYLLGSALEFTDK-GMSPSTRKIYEKIREKVEK
17	SWALL: BAB29407	38.6%	SKALCHPSSVDSIPT SANQEDHVS MGWGAARKALRVVEHVEQVLAIELLAACQGI EFLRPLKTTT PLEKVYDLVRSVVRP
18	SWALL: HUTH_RAT	38.6%	SKALCHPSSVDSIPT SANQEDHVS MGWGAARKALRVIEHVEQVLAIELLAACQGI EFLRPLKTTT PLEKVYDLVRSVVRP
19	SWALL: AAG53586	38.2%	NKGLCHPTSVDK-PPSANQEDHVS MAPAAGRRLWEMAGNTRGVLAIEWLAACQGLDGLTSSPLLEQARQSCGEQVAH
20	SWALL: Q9KKE0	39.8%	NRRLAAPASLDGGITSA LQEDMLTHATPAAWKALSIVDNLERILAIELLAAHRPMSCSRKRARRRNAPLPFTGTIARRSP
21	SWALL: Q9HQD5	38.9%	LRSLGQP-TLDNASVSGAQEDHVS SMSAGAAYNFREAVEKEAATVVGVELL CGAQGREFLDPLALGAGTAAAYDLVR-EVSE

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Figure 14 ^G cont'd.

	481		5	513
983831	100.0%		PGQDRFLSAELEAAYDLLANGSVHKALEAHLPA	
1 SWALL: CAC21618	66.1%		PGPDRHLAPDLAAADAFVVRAGHLVAAAE SVTGP	
2 SWALL: HUTH_STRGR	65.4%		PGPDRFLAPDLAAADTFVREGRLVAAVEPVTGP	
3 SWALL: HUTH_DEIRA	46.8%		LTEDRYFRPDLRLRGELVSGRVAQAADTQAPA	
4 SWALL: BAB16159	42.0%		LEDDRYMATDLKAAIEVVASGALVSAISSGLPV	
5 SWALL: Q9KWE4	42.0%		LEDDRYMATDLKAAIEVVASGALVSAISSGLPV	
6 SWALL: HUTH_BACSU	40.4%		IQQDRVFSYDIERLTDWLKESLIPDHQNKELR	
7 SWALL: Q9KSQ4	42.2%		YKDRYFAPDIEKANALL-QLAVHNRLMPDQLL	
8 SWALL: Q9HU85	41.7%		YQEDRFFAPDIEAASQLLASGCLNALLPARLLP	
9 SWALL: Q9KBE6	39.3%		IDQDRMFAKDIERAAKWLDGSDWDFTKMREKER	
10 SWALL: HUTH_PSEPU	41.7%		YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS	
11 SWALL: HUTH_RHIME	40.6%		IEEDRYMADDLKAAGDLVASGRLAAAVSAGLPK	
12 SWALL: Q9HU90	40.7%		YDTRWLAPDIAASAAAILGERKSLARLAASIGD	
13 SWALL: HUTH_HUMAN	39.2%		WIKDRFMAPDIEAAHRLLLLEQKVWEVAAPYIEK	
14 SWALL: HUTH_CAEEL	38.8%		PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET	
15 SWALL: Q9HLI6	41.0%		LDHDRPPSFDIETIRKMMDKKEFISALP-----	
16 SWALL: HUTH_MOUSE	38.6%		WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK	
17 SWALL: BAB29407	38.6%		WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK	
18 SWALL: HUTH_RAT	38.2%		WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK	
19 SWALL: AAG53586	39.8%		YDDDRFFAPDIEAAISLLNKGSLVGLLP AFL--	
20 SWALL: Q9KKE0	38.9%		PIATIVR-----	
21 SWALL: Q9HQD5	42.2%		PAGDRALADDMAAVGDLVRAGLVEDAVARALDA	



Figure 14 ⁴ ~~cont'd~~

KEY:

983831	:	HAL
1 CAC21618	:	Streptomyces coelicolor
2 HUTH_STRGR	:	Streptomyces griseus
3 HUTH_DEIRA	:	Deinococcus radiodurans
4 BAB16159	:	Agrobacterium rhizogenes
5 Q9KWE4	:	Agrobacterium rhizogenes
6 HUTH_BACSU	:	Bacillus subtilis
7 Q9KSQ4	:	Vibrio cholerae
8 Q9HU85	:	Pseudomonas aeruginosa
9 Q9KBE6	:	Bacillus halodurans
10 HUTH_PSEPU	:	Pseudomonas putida
11 HUTH_RHIME	:	Rhizobium meliloti
12 Q9HU90	:	Pseudomonas aeruginosa
13 HUTH_HUMAN	:	Human
14 HUTH_CAEEL	:	Caenorhabditis elegans
15 Q9HLI6	:	Thermoplasma acidophilum
16 HUTH_MOUSE	:	Mouse
17 BAB29407	:	Mus musculus (Mouse)
18 HUTH_RAT	:	Rat
18 AAG53586	:	uncultured bacterium pCosAS1
20 Q9KKE0	:	Rhizobium meliloti
21 Q9HQD5	:	Halobacterium sp

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Figure 15 A.

```
STRG      6  VVVGTS GTTAEDV VAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGAL
"HAL"     7  ITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGISTGFGAL
          *  ** ** ** ** ** ** ** ** ** ** ** ** ** **   *  ** **   *  ** **   *  ** **   *  ** **   *
STRG,    66  ASRHIGTELRAQLQRNIVRSHAAGMGPVEREVVRALMFLRLKTVASGHTGVRPEVAQTM
HAL      67  ATRHIAPEDRAKLQRSLIRSHAAGMGEPPVEREVVRALMFLRAKTLASGRTGVRPVPVLETM
          *  ** *  *  ** **   *  ** ** ** ** **   *  ** **   *  ** **   *  **
STRG     126  ADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDGTVRPAGELLAAHGIA
HAL      127  VGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHGDIRPVPELFAEAGLT
          *  ** ** ** **   *  ** ** **   *  ** ** **   *  ** **   *  **
STRG     186  PVELREKEGLALLNGTDGMLGMLMALADLRNLYTSADITAAALSLEALLGTDKVLAPELH
HAL      187  PVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQVFRAELH
          *  ** ** **   *  ** ** **   *  ** ** **   *  ** **   *  **
STRG     246  A-IRPHPGQGVSA DNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAA
HAL      247  EPLRPHPGQGRSAQNMF AFLADSPIVASHREGDGRVQDAYSLRCS PQVTGAARDTIAHAR
          *  ** ** **   *  ** ** **   *  ** ** **   *  ** **   *  **
STRG     305  LVAGRELASSVDNPVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTDRLDD
HAL      307  LVATRELA AAI DNPNVLPDSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRLMD
          *  ** ** **   *  ** ** **   *  ** ** **   *  ** **   *  **
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OIPF

Figure 15^B Cont'd.

STRG	365	KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSI	IPSSAMQEDHVS	MG	
HAL	367	PARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAVPASVDSI	IPSSAMQEDHVS	LG	
		** ** *	** ** *	*	
STRG	425	WSAARKLRTAVDNLARI	VAVELYAA	TRAIELRAAEGLTPAPASEAVVAALRAAGAE	GPGP
HAL	427	WHAARKLRTSVANLRRILAVEMLI	AGRALDLRAP--	LKPGPATGAVLEVLRSKVA--	GPGQ
		* * * * *	* * * * *	* * * * *	* * * * *
STRG	485	DRFLAPDLAAADTFVREGRL	VAAVE		
HAL	484	DRFLSAELEEAAAYDLLANGSV	HKALE		
		* * * * *	* * * * *	* * * * *	* * * * *